

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/016,481

DATE: 01/03/2002
TIME: 15:33:25

Input Set : A:\Uc5016.txt
Output Set: N:\CRF3\01032002\J016481.raw

ENTERED

OK

4 <110> APPLICANT: Zhou, Qun-Yong
5 Ehlert, Frederick
7 <120> TITLE OF INVENTION: Prokineticin Polypeptides, Related
8 Compositions and Methods
10 <130> FILE REFERENCE: P-UC 5016
12 <140> CURRENT APPLICATION NUMBER: US/10/016,481
12 <141> CURRENT FILING DATE: 2001-11-01
12 <150> PRIOR APPLICATION NUMBER: 60/245,882
13 <151> PRIOR FILING DATE: 2000-11-03
15 <160> NUMBER OF SEQ ID NOS: 19
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1377
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (55)...(369)
28 <400> SEQUENCE: 1
29 ggggaagcga gaggcaccta agcaggcagt gttttgcctt caccccaagt gacc atg 57
30 Met
31 1
33 aga ggt gcc acg cga gtc tca atc atg ctc ctc cta gta act gtg tct, 105
34 Arg Gly Ala Thr Arg Val Ser Ile Met Leu Leu Leu Val Thr Val Ser
35 5 10 15
37 gac tgt gct gtg atc aca ggg gcc tgt gag cgg gat gtc cag tgt ggg 153
38 Asp Cys Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val Gln Cys Gly
39 20 25 30
41 gca ggc acc tgc tgt gcc atc agc ctg tgg ctt cga ggg ctg cgg atg 201
42 Ala Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg Met
43 35 40 45
45 tgc acc ccg ctg ggg cgg gaa ggc gag gag tgc cac ccc ggc agc cac 249
46 Cys Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser His
47 50 55 60 65
49 aag gtc ccc ttc ttc agg aaa cgc aag cac cac acc tgt cct tgc ttg 297
50 Lys Val Pro Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys Leu
51 70 75 80
53 ccc aac ctg ctg tgc tcc agg ttc ccg gac ggc agg tac cgc tgc tcc 345
54 Pro Asn Leu Leu Cys Ser Arg Phe Pro Asp Gly Arg Tyr Arg Cys Ser
55 85 90 95
57 atg gac ttg aag aac atc aat ttt taggcgcttg cctggtctca ggataccac 399
58 Met Asp Leu Lys Asn Ile Asn Phe
59 100 105
61 catccttttc tgagcacagc ctggattttt atttctgcca tgaaaccag ctcccatgac 459
62 tctccagtc cctacactga ctaccctgat ctctctgtc tagtacgcac atatgcacac 519
63 aggcagacat acctcccatc atgacatggt cccaaggctg gcctgaggat gtcacagctt 579
64 gaggctgtgg tgtgaaagggt ggccagcctg gttctcttcc ctgctcaggc tgccagagag 639

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TECH CENTER 1600/2900

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65 gtggtaaatg gcagaaagga cattccccct cccctcccca ggtgacctgc tctctttcct 699
66 gggccctgcc cctctcccca catgtatccc tcggtctgaa ttagacattc ctgggcacag 759
67 gctcttggtg gcattgctca gagtcccagg tccctggcctg accctcaggc ccttcacgtg 819
68 aggtctgtga ggaccaatgt gtgggtagtt catcttcctt cgattgggta actccttagt 879
69 ttcagaccac agactcaaga ttggctcttc ccagagggca gcagacagtc accccaaggc 939
70 aggtgtaggg agcccaggga ggccaatcag cccctgaag actctggtcc cagtcagcct 999
71 gtggcttggt gcctgtgacc tgtgaccttc tgccagaatt gtcatgcctc tgaggccccc 1059
72 tcttaccaca ctttaccagt taaccactga agcccccaat tcccacagct tttccattaa 1119
73 aatgcaaatg gtggtggttc aatctaatt gatattgaca tattagaagg caattagggt 1179
74 gtttccttaa acaactcctt tccaaggatc agccctgaga gcaggttggt gactttgagg 1239
75 agggcagtc tctgtccaga ttgggggtgg agcaagggac agggagcagg gcaggggctg 1299
76 aaaggggcac tgattcagac cagggaggca actacacacc aacctgctgg ctttagaata 1359
77 aaagcaccaa ctgaactg                                     1377

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79 <210> SEQ ID NO: 2

80 <211> LENGTH: 105

81 <212> TYPE: PRT

82 <213> ORGANISM: Homo sapiens

84 <400> SEQUENCE: 2

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85 Met Arg Gly Ala Thr Arg Val Ser Ile Met Leu Leu Leu Val Thr Val
86 1 5 10 15
87 Ser Asp Cys Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val Gln Cys
88 20 25 30
89 Gly Ala Gly Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg
90 35 40 45
91 Met Cys Thr Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser
92 50 55 60
93 His Lys Val Pro Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys
94 65 70 75 80
95 Leu Pro Asn Leu Leu Cys Ser Arg Phe Pro Asp Gly Arg Tyr Arg Cys
96 85 90 95
97 Ser Met Asp Leu Lys Asn Ile Asn Phe
98 100 105

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101 <210> SEQ ID NO: 3

102 <211> LENGTH: 86

103 <212> TYPE: PRT

104 <213> ORGANISM: Homo sapiens

106 <400> SEQUENCE: 3

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107 Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Val Gln Cys Gly Ala Gly
108 1 5 10 15
109 Thr Cys Cys Ala Ile Ser Leu Trp Leu Arg Gly Leu Arg Met Cys Thr
110 20 25 30
111 Pro Leu Gly Arg Glu Gly Glu Glu Cys His Pro Gly Ser His Lys Val
112 35 40 45
113 Pro Phe Phe Arg Lys Arg Lys His His Thr Cys Pro Cys Leu Pro Asn
114 50 55 60
115 Leu Leu Cys Ser Arg Phe Pro Asp Gly Arg Tyr Arg Cys Ser Met Asp
116 65 70 75 80
117 Leu Lys Asn Ile Asn Phe
118 85

```

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121 <210> SEQ ID NO: 4
122 <211> LENGTH: 1406
123 <212> TYPE: DNA
124 <213> ORGANISM: Homo sapiens
126 <220> FEATURE:
127 <221> NAME/KEY: CDS
128 <222> LOCATION: (10)...(333)
130 <400> SEQUENCE: 4
131 gagggcgcc atg agg agc ctg tgc tgc gcc cca ctc ctg ctc ctc ttg ctg 51
132           Met Arg Ser Leu Cys Cys Ala Pro Leu Leu Leu Leu Leu
133           1           5           10
135 ctg ccg ccg ctg ctg ctc acg ccc cgc gct ggg gac gcc gcc gtg atc 99
136 Leu Pro Pro Leu Leu Leu Thr Pro Arg Ala Gly Asp Ala Ala Val Ile
137 15           20           25           30
139 acc ggg gct tgt gac aag gac tcc caa tgt ggt gga ggc atg tgc tgt 147
140 Thr Gly Ala Cys Asp Lys Asp Ser Gln Cys Gly Gly Gly Met Cys Cys
141           35           40           45
143 gct gtc agt atc tgg gtc aag agc ata agg att tgc aca cct atg ggc 195
144 Ala Val Ser Ile Trp Val Lys Ser Ile Arg Ile Cys Thr Pro Met Gly
145           50           55           60
147 aaa ctg gga gac agc tgc cat cca ctg act cgt aaa gtt cca ttt ttt 243
148 Lys Leu Gly Asp Ser Cys His Pro Leu Thr Arg Lys Val Pro Phe Phe
149           65           70           75
151 ggg cgg agg atg cat cac act tgc cca tgt ctg cca ggc ttg gcc tgt 291
152 Gly Arg Arg Met His His Thr Cys Pro Cys Leu Pro Gly Leu Ala Cys
153           80           85           90
155 tta cgg act tca ttt aac cga ttt att tgt tta gcc caa aag 333
156 Leu Arg Thr Ser Phe Asn Arg Phe Ile Cys Leu Ala Gln Lys
157 95           100           105
159 taatcgctct ggagtagaaa ccaaagtga atagccacat cttacctgta aagtcttact 393
160 tgtgattgtg ccaaacaaaa aatgtgccag aaagaaatgc tcttgcttcc tcaactttcc 453
161 aagtaacatt tttatctttg atttgtaaat gatttttttt ttttttttta tcgaaagaga 513
162 attttacttt tggatagaaa tatgaagtgt aaggcattat ggaactgggt cttattttccc 573
163 tgtttgtgtt ttggtttgat ttggcttttt tcttaaattgt caaaaacgta cccatttttca 633
164 caaaaatgag gaaaataaga atttgatatt ttgttagaaa aacttttttt tttttttctc 693
165 accaccccaa gccccatttg tgccctgccg cacaaatata cctacagctt ttggtccctt 753
166 gcctcttcca cctcaaagaa tttcaaggct cttaccttac tttatttttg tccattttctc 813
167 ttccctcctc ttgcatttta aagtggaggg tttgtctctt tgagtttgat ggcagaatca 873
168 ctgatgggaa tccagctttt tgctggcatt taaatagtga aaagagtgtg tatgtgaact 933
169 tgacactcca aactcctgtc atggcacgga agctaggagt gctgctggac ccttcctaaa 993
170 cctgtcactc aagaggactt cagctctgct gttgggctgg tgtgtggaca gaaggaatgg 1053
171 aaagccaaat taatttagtc cagatttcta ggtttgggtt tttctaaaaa taaaagatta 1113
172 catttacttc ttttactttt tataaagttt tttttcctta gtctcctact tagagatatt 1173
173 ctagaaaatg tcaactgaag aggaagtatt tattttaatc tggcacaaca ctaattacca 1233
174 tttttaaagc ggtattaagt tgtaatttaa accttgtttg taactgaaag gtcgattgta 1293
175 atggattgcc gtttgtaact gtatcagtat tgctgtgtaa aaattctgta tcagaataat 1353
176 aacagtactg tatatcattt gatatttttt aatattatat cctatttttt gtc 1406
178 <210> SEQ ID NO: 5
179 <211> LENGTH: 108

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180 <212> TYPE: PRT
181 <213> ORGANISM: Homo sapiens
183 <400> SEQUENCE: 5
184 Met Arg Ser Leu Cys Cys Ala Pro Leu Leu Leu Leu Leu Leu Pro
185 1 5 10 15
186 Pro Leu Leu Leu Thr Pro Arg Ala Gly Asp Ala Ala Val Ile Thr Gly
187 20 25 30
188 Ala Cys Asp Lys Asp Ser Gln Cys Gly Gly Gly Met Cys Cys Ala Val
189 35 40 45
190 Ser Ile Trp Val Lys Ser Ile Arg Ile Cys Thr Pro Met Gly Lys Leu
191 50 55 60
192 Gly Asp Ser Cys His Pro Leu Thr Arg Lys Val Pro Phe Phe Gly Arg
193 65 70 75 80
194 Arg Met His His Thr Cys Pro Cys Leu Pro Gly Leu Ala Cys Leu Arg
195 85 90 95
196 Thr Ser Phe Asn Arg Phe Ile Cys Leu Ala Gln Lys
197 100 105
200 <210> SEQ ID NO: 6
201 <211> LENGTH: 81
202 <212> TYPE: PRT
203 <213> ORGANISM: Homo sapiens
205 <400> SEQUENCE: 6
206 Ala Val Ile Thr Gly Ala Cys Asp Lys Asp Ser Gln Cys Gly Gly Gly
207 1 5 10 15
208 Met Cys Cys Ala Val Ser Ile Trp Val Lys Ser Ile Arg Ile Cys Thr
209 20 25 30
210 Pro Met Gly Lys Leu Gly Asp Ser Cys His Pro Leu Thr Arg Lys Val
211 35 40 45
212 Pro Phe Phe Gly Arg Arg Met His His Thr Cys Pro Cys Leu Pro Gly
213 50 55 60
214 Leu Ala Cys Leu Arg Thr Ser Phe Asn Arg Phe Ile Cys Leu Ala Gln
215 65 70 75 80
216 Lys
220 <210> SEQ ID NO: 7
221 <211> LENGTH: 21
222 <212> TYPE: PRT
223 <213> ORGANISM: Homo sapiens
225 <400> SEQUENCE: 7
226 Asn Asn Phe Gly Asn Gly Arg Gln Glu Arg Arg Lys Arg Lys Arg Ser
227 1 5 10 15
228 Lys Arg Lys Lys Glu
229 20
232 <210> SEQ ID NO: 8
233 <211> LENGTH: 21
234 <212> TYPE: PRT
235 <213> ORGANISM: Homo sapiens
237 <400> SEQUENCE: 8
238 Ser His Val Ala Asn Gly Arg Gln Glu Arg Arg Arg Ala Lys Arg Arg
239 1 5 10 15

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240 Lys Arg Lys Lys Glu
241           20
244 <210> SEQ ID NO: 9
245 <211> LENGTH: 19
246 <212> TYPE: PRT
247 <213> ORGANISM: Homo sapiens
249 <400> SEQUENCE: 9
250 Met Arg Gly Ala Thr Arg Val Ser Ile Met Leu Leu Leu Val Thr Val
251 1           5           10           15
252 Ser Asp Cys
256 <210> SEQ ID NO: 10
257 <211> LENGTH: 26
258 <212> TYPE: PRT
259 <213> ORGANISM: Homo sapiens
261 <400> SEQUENCE: 10
262 Met Arg Ser Leu Cys Cys Ala Pro Leu Leu Leu Leu Leu Leu Pro
263 1           5           10           15
264 Leu Leu Leu Thr Pro Pro Ala Gly Asp Ala
265           20           25
268 <210> SEQ ID NO: 11
269 <211> LENGTH: 96
270 <212> TYPE: PRT
271 <213> ORGANISM: Bombina variegata
273 <400> SEQUENCE: 11
274 Met Lys Cys Phe Ala Gln Ile Val Val Leu Leu Leu Val Ile Ala Phe
275 1           5           10           15
276 Ser His Gly Ala Val Ile Thr Gly Ala Cys Asp Lys Asp Val Gln Cys
277           20           25           30
278 Gly Ser Gly Thr Cys Cys Ala Ala Ser Ala Trp Ser Arg Asn Ile Arg
279           35           40           45
280 Phe Cys Ile Pro Leu Gly Asn Ser Gly Glu Asp Cys His Pro Ala Ser
281           50           55           60
282 His Lys Val Pro Tyr Asp Gly Lys Arg Leu Ser Ser Leu Cys Pro Cys
283 65           70           75           80
284 Lys Ser Gly Leu Thr Cys Ser Lys Ser Gly Glu Lys Phe Lys Cys Ser
285           85           90           95
288 <210> SEQ ID NO: 12
289 <211> LENGTH: 81
290 <212> TYPE: PRT
291 <213> ORGANISM: Dendroaspis polylepis polylepis
293 <400> SEQUENCE: 12
294 Ala Val Ile Thr Gly Ala Cys Glu Arg Asp Leu Gln Cys Gly Lys Gly
295 1           5           10           15
296 Thr Cys Cys Ala Val Ser Leu Trp Ile Lys Ser Val Arg Val Cys Thr
297           20           25           30
298 Pro Val Gly Thr Ser Gly Glu Asp Cys His Pro Ala Ser His Lys Ile
299           35           40           45
300 Pro Phe Ser Gly Gln Arg Lys Met His His Thr Cys Pro Cys Ala Pro
301           50           55           60

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VERIFICATION SUMMARY

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.L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date